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Wed Nov 21 09:16:51 2001 [BLASTN 2.2.1 [Jul-12-2001], NCBI]
Repeats masked (summary below)
/home/ruby/va/Molbio/carpanda/tempblast/ss.DNA59820 (2988 bp)

Sequences producing High-scoring Segment Pairs:				Frame	Score	Match
Pct	E-val					
1	P_AAZ65074	Membrane-bound protein PRO1281 encoding		+	2988	2988
100	0.0					
2	P_AAF44220	Human PRO1281 (UNQ651) nucleotide sequen		+	2988	2988
100	0.0					
3	P_AAC58388	Human PRO1281 nucleotide sequence SEQ ID		+	2980	2987
100	0.0					
4	P_AAC69800	Human breast tumour antigen coding seque		+	2487	2502
100	0.0					

>1 P_AAZ65074 Membrane-bound protein PRO1281 encoding cDNA. (2988 bp) [1 seg]

Score = 2988 (5923 bits), Expect = 0.0

Identities = 2988/2988 (100%), at 1,1-2988,2988, Strand +/+

ss.DNA59820 1
GCCGAGCGCAAGAACCCTGCGCAGCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGC

P_AAZ65074 1
GCCGAGCGCAAGAACCCTGCGCAGCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGC

ss.DNA59820 61
TCCGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCCGCCCGC

P_AAZ65074 61
TCCGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCCGCCCGC

ss.DNA59820 121
GGGGCCCGAGCCCTCCGGATCCGCCCCCTCCCCGGTCCCGCCCCCTCGGAGACTCCTCTG

P_AAZ65074 121
GGGGCCCGAGCCCTCCGGATCCGCCCCCTCCCCGGTCCCGCCCCCTCGGAGACTCCTCTG

ss.DNA59820 181
GCTGCTCTGGGGGTTCCGCCGGGGCCGGGGACCCGCGGTCCGGGCGCCATGCGGGCATCGC

P_AAZ65074 181
GCTGCTCTGGGGGTTCCGCCGGGGCCGGGGACCCGCGGTCCGGGCGCCATGCGGGCATCGC

ss.DNA59820 241
TGCTGCTGTGCGGTGCTGCGGCCCCGAGGGCCCCGTGGCCGTGGGCATCTCCCTGGGCTTCA

P_AAZ65074 241
TGCTGCTGTGCGGTGCTGCGGCCCCGAGGGCCCCGTGGCCGTGGGCATCTCCCTGGGCTTCA

ss.DNA59820 301
CCCTGAGCCTGCTCAGCGTCACCTGGGTGGAGGAGCCGTGCGGCCCCAGGCCCCCCCCAAC

BLAST RESULTS A-1

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*****
P_AAZ65074      301
CCTTGAGCCTGCTCAGCGTCACCTGGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCAAC

ss.DNA59820     361
CTGGAGACTCTGAGCTGCCGCCGCGGGCAACACCAACGCGGCGCGCCGCCCCAACTCGG

*****
P_AAZ65074      361
CTGGAGACTCTGAGCTGCCGCCGCGGGCAACACCAACGCGGCGCGCCGCCCCAACTCGG

ss.DNA59820     421
TGCAGCCCGGAGCGGAGCGCGAGAAGCCCGGGGCGGCGAAGGCGCCGGGAGAATTGGG

*****
P_AAZ65074      421
TGCAGCCCGGAGCGGAGCGCGAGAAGCCCGGGGCGGCGAAGGCGCCGGGAGAATTGGG

ss.DNA59820     481
AGCCGCGCGTCTTGCCCTACCACCTGCACAGCCCGGCCAGGCCGCCAAAAGGCCGTCA

*****
P_AAZ65074      481
AGCCGCGCGTCTTGCCCTACCACCTGCACAGCCCGGCCAGGCCGCCAAAAGGCCGTCA

ss.DNA59820     541
GGACCCGCTACATCAGCACGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGA

*****
P_AAZ65074      541
GGACCCGCTACATCAGCACGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGA

ss.DNA59820     601
CCTCTCAGACCACGCTGCCCACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGC

*****
P_AAZ65074      601
CCTCTCAGACCACGCTGCCCACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGC

ss.DNA59820     661
TGGAGCGTGTGGTGTTCCTGACGGGCGCACGGGGCCGCCGGGCCCCACCTGGCATGGCAG

*****
P_AAZ65074      661
TGGAGCGTGTGGTGTTCCTGACGGGCGCACGGGGCCGCCGGGCCCCACCTGGCATGGCAG

ss.DNA59820     721
TGGTGACGCTGGGCGAGGAGCGACCCATTGGACACCTGCACCTGGCGCTGCGCCACCTGC

*****
P_AAZ65074      721
TGGTGACGCTGGGCGAGGAGCGACCCATTGGACACCTGCACCTGGCGCTGCGCCACCTGC

ss.DNA59820     781
TGGAGCAGCACGGCGACGACTTTGACTGGTTCTTCCTGGTGCCTGACACCACCTACACCG

*****
P_AAZ65074      781
TGGAGCAGCACGGCGACGACTTTGACTGGTTCTTCCTGGTGCCTGACACCACCTACACCG

ss.DNA59820     841

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BLAST RESULT A2

AGGCGCACGGCCTGGCAGCCTAACTGGCCACCTCAGCCTGGCCTCCGCCGCCACCTGT

P_AAZ65074 841
AGGCGCACGGCCTGGCAGCCTAACTGGCCACCTCAGCCTGGCCTCCGCCGCCACCTGT
ss.DNA59820 901
ACCTGGGCCGGCCCCAGGACTTCATCGGCGGAGAGCCCACCCCGGCCGCTACTGCCACG

P_AAZ65074 901
ACCTGGGCCGGCCCCAGGACTTCATCGGCGGAGAGCCCACCCCGGCCGCTACTGCCACG
ss.DNA59820 961
GAGGCTTTGGGGTGCTGCTGTCGCGCATGCTGCTGCAACAACCTGCGCCCCACCTGGAAG

P_AAZ65074 961
GAGGCTTTGGGGTGCTGCTGTCGCGCATGCTGCTGCAACAACCTGCGCCCCACCTGGAAG
ss.DNA59820 1021
GCTGCCGCAACGACATCGTCAGTGCGCGCCCTGACGAGTGGCTGGGTGCTGCATTCTCG

P_AAZ65074 1021
GCTGCCGCAACGACATCGTCAGTGCGCGCCCTGACGAGTGGCTGGGTGCTGCATTCTCG
ss.DNA59820 1081
ATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGGGGGTGCATATAGCCATCTGGAGC

P_AAZ65074 1081
ATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGGGGGTGCATATAGCCATCTGGAGC
ss.DNA59820 1141
TGAGCCCTGGGGAGCCAGTGCAGGAGGGGGACCCTCATTTCCGAAGTGCCCTGACAGCCC

P_AAZ65074 1141
TGAGCCCTGGGGAGCCAGTGCAGGAGGGGGACCCTCATTTCCGAAGTGCCCTGACAGCCC
ss.DNA59820 1201
ACCCTGTGCGTGACCCTGTGCACATGTACCAGCTGCACAAAGCTTTCGCCCCGAGCTGAAC

P_AAZ65074 1201
ACCCTGTGCGTGACCCTGTGCACATGTACCAGCTGCACAAAGCTTTCGCCCCGAGCTGAAC
ss.DNA59820 1261
TGGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGATCCAGAATACCAGCCATC

P_AAZ65074 1261
TGGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGATCCAGAATACCAGCCATC
ss.DNA59820 1321
TGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATTCCAGCACCATCCCGCC

P_AAZ65074 1321
TGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATTCCAGCACCATCCCGCC

Blast Results A-3

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ss.DNA59820 1381
CGGCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCAGCACGCTTCTCCT
*****
P_AAZ65074 1381
CGGCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCAGCACGCTTCTCCT

ss.DNA59820 1441
GCGCCGATGGCTCACCCCGCTGCCCACTGCGTGGGGCTGACCGGGCTGATGTGGCCGATG
*****
P_AAZ65074 1441
GCGCCGATGGCTCACCCCGCTGCCCACTGCGTGGGGCTGACCGGGCTGATGTGGCCGATG

ss.DNA59820 1501
TTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCGGCCCTTGCGGCTCCAGA
*****
P_AAZ65074 1501
TTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCGGCCCTTGCGGCTCCAGA

ss.DNA59820 1561
AGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGAATACACGC
*****
P_AAZ65074 1561
AGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGAATACACGC

ss.DNA59820 1621
TGGACTTGACAGCTGGAGGCACTGACCCCCAGGGAGGCCCGGCCCTCACTCGCCGAG
*****
P_AAZ65074 1621
TGGACTTGACAGCTGGAGGCACTGACCCCCAGGGAGGCCCGGCCCTCACTCGCCGAG

ss.DNA59820 1681
TGCAGCTGCTCCGGCCGCTGAGCCGCTGGAGATCTTGCTGTGCCCTATGTCACTGAGG
*****
P_AAZ65074 1681
TGCAGCTGCTCCGGCCGCTGAGCCGCTGGAGATCTTGCTGTGCCCTATGTCACTGAGG

ss.DNA59820 1741
CCTCACGTCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGGCT
*****
P_AAZ65074 1741
CCTCACGTCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGGCT

ss.DNA59820 1801
TCTTGAGGCCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC
*****
P_AAZ65074 1801
TCTTGAGGCCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC

ss.DNA59820 1861
TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATGCAGATGTCTTCGCAC
*****

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BLAST RESULTS A-4

P_AAZ65074 1861
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGGCCCATGCAGATGTCTTCGCAC

 ss.DNA59820 1921
 CTGTCAAGGCCACGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGGTGCCATGGC

 P_AAZ65074 1921
 CTGTCAAGGCCACGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGGTGCCATGGC

 ss.DNA59820 1981
 TCAGTGTGCAGACAGCCGCACCCCTCACCCTGCGCCTCATGGATCTACTCTCCAAGAAGC

 P_AAZ65074 1981
 TCAGTGTGCAGACAGCCGCACCCCTCACCCTGCGCCTCATGGATCTACTCTCCAAGAAGC

 ss.DNA59820 2041
 ACCCGCTGGACACACTGTTCTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCC

 P_AAZ65074 2041
 ACCCGCTGGACACACTGTTCTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCC

 ss.DNA59820 2101
 TGAACCGCTGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTCC

 P_AAZ65074 2101
 TGAACCGCTGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTCC

 ss.DNA59820 2161
 AAGCCTTCCACCCAGGTGTGGCCCCACCACAAGGGCCTGGGCCCCCAGAGCTGGGCCGTG

 P_AAZ65074 2161
 AAGCCTTCCACCCAGGTGTGGCCCCACCACAAGGGCCTGGGCCCCCAGAGCTGGGCCGTG

 ss.DNA59820 2221
 AACTGGCCGCTTTGATCGCCAGGCAGCCAGCGAGGCCTGCTTCTACAACCTCCGACTACG

 P_AAZ65074 2221
 AACTGGCCGCTTTGATCGCCAGGCAGCCAGCGAGGCCTGCTTCTACAACCTCCGACTACG

 ss.DNA59820 2281
 TGGCAGCCCGTGGGCGCCTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCC

 P_AAZ65074 2281
 TGGCAGCCCGTGGGCGCCTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCC

 ss.DNA59820 2341
 TGGATGTGTACGAGCTGTTCTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGC

 P_AAZ65074 2341
 TGGATGTGTACGAGCTGTTCTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGC

 ss.DNA59820 2401
 CGGCGCTGCTGCAGCGCTACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGT

Blast Results A-5

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*****
P_AAZ65074 2401
CGGCGCTGCTGCAGCGCTACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGT

ss.DNA59820 2461
ACCACCGCTGCCTCCAGAGCGTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGC

*****
P_AAZ65074 2461
ACCACCGCTGCCTCCAGAGCGTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGC

ss.DNA59820 2521
TACTCTTTGAACAGGAGCAGGGCAACAGCACCTGACCCACCCCTGTCCCCGTGGGCCGTG

*****
P_AAZ65074 2521
TACTCTTTGAACAGGAGCAGGGCAACAGCACCTGACCCACCCCTGTCCCCGTGGGCCGTG

ss.DNA59820 2581
GCATGGCCACACCCACCCCACTTCTCCCCAAAACCAGAGCCACCTGCCAGCCTCGCTG

*****
P_AAZ65074 2581
GCATGGCCACACCCACCCCACTTCTCCCCAAAACCAGAGCCACCTGCCAGCCTCGCTG

ss.DNA59820 2641
GGCAGGGCTGGCCGTAGCCAGACCCCAAGCTGGCCCACTGGTCCCCTCTCTGGCTCTGTG

*****
P_AAZ65074 2641
GGCAGGGCTGGCCGTAGCCAGACCCCAAGCTGGCCCACTGGTCCCCTCTCTGGCTCTGTG

ss.DNA59820 2701
GGTCCCTGGGCTCTGGACAAGCACTGGGGGACGTGCCCCAGAGCCACCCACTTCTCATC

*****
P_AAZ65074 2701
GGTCCCTGGGCTCTGGACAAGCACTGGGGGACGTGCCCCAGAGCCACCCACTTCTCATC

ss.DNA59820 2761
CCAAACCCAGTTTCCCTGCCCCCTGACGCTGCTGATTCTGGGCTGTGGCCTCCACGTATTT

*****
P_AAZ65074 2761
CCAAACCCAGTTTCCCTGCCCCCTGACGCTGCTGATTCTGGGCTGTGGCCTCCACGTATTT

ss.DNA59820 2821
ATGCAGTACAGTCTGCCTGACGCCAGCCCTGCCTCTGGGCCCTGGGGGCTGGGCTGTAGA

*****
P_AAZ65074 2821
ATGCAGTACAGTCTGCCTGACGCCAGCCCTGCCTCTGGGCCCTGGGGGCTGGGCTGTAGA

ss.DNA59820 2881
AGAGTTGTTGGGAAGGAGGGAGCTGAGGAGGGGGCATCTCCCAACTTCTCCCTTTTGA

*****
P_AAZ65074 2881
AGAGTTGTTGGGAAGGAGGGAGCTGAGGAGGGGGCATCTCCCAACTTCTCCCTTTTGA

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BLAST RESULTS A-U

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ss.DNA59820 2941 CCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCAAGTGTGGAAAAA
*****
P_AAZ65074 2941 CCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCAAGTGTGGAAAAA

>2 P_AAF44220 Human PRO1281 (UNQ651) nucleotide sequence SEQ ID NO:325.
(2988 bp) [1 seg]
Score = 2988 (5923 bits), Expect = 0.0
Identities = 2988/2988 (100%), at 1,1-2988,2988, Strand +/+

ss.DNA59820 1
GCCGAGCGCAAGAACCCTGCGCAGCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGC
*****
P_AAF44220 1
GCCGAGCGCAAGAACCCTGCGCAGCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGC

ss.DNA59820 61
TCCGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCCGC
*****
P_AAF44220 61
TCCGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCCGC

ss.DNA59820 121
GGGGCCCGAGCCCTCCGATCCGCCCCCTCCCCGGTCCCGCCCCCTCGGAGACTCCTCTG
*****
P_AAF44220 121
GGGGCCCGAGCCCTCCGATCCGCCCCCTCCCCGGTCCCGCCCCCTCGGAGACTCCTCTG

ss.DNA59820 181
GCTGCTCTGGGGGTTGCGCGGGGCCGGGGACCCGCGGTCCGGGCGCCATGCGGGCATCGC
*****
P_AAF44220 181
GCTGCTCTGGGGGTTGCGCGGGGCCGGGGACCCGCGGTCCGGGCGCCATGCGGGCATCGC

ss.DNA59820 241
TGCTGCTGTGCGGTGCTGCGGCCCGCAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTCA
*****
P_AAF44220 241
TGCTGCTGTGCGGTGCTGCGGCCCGCAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTCA

ss.DNA59820 301
CCCTGAGCCTGCTCAGCGTCACCTGGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCCAAC
*****
P_AAF44220 301
CCCTGAGCCTGCTCAGCGTCACCTGGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCCAAC

ss.DNA59820 361
CTGGAGACTCTGAGCTGCCGCCGCGCGGCAACACCAACGCGGCGCGCCGGCCCAACTCGG
*****
P_AAF44220 361
CTGGAGACTCTGAGCTGCCGCCGCGCGGCAACACCAACGCGGCGCGCCGGCCCAACTCGG

ss.DNA59820 421
TGCAGCCCGGAGCGGAGCGGAGAAGCCCGGGCCGGCGAAGGCGCCGGGGAGAATTGGG

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BLAST RESULTS A-7

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*****
P_AAF44220      421
TGCAGCCCGGAGCGGAGCGCGAGAAGCCCGGGGCCGCGAAGGCGCCGGGGAGAATTGGG

ss.DNA59820      481
AGCCGCGCGTCTTGCCCTACCACTGTCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTCA

*****
P_AAF44220      481
AGCCGCGCGTCTTGCCCTACCACTGTCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTCA

ss.DNA59820      541
GGACCCGCTACATCAGCACGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGA

*****
P_AAF44220      541
GGACCCGCTACATCAGCACGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGA

ss.DNA59820      601
CCTCTCAGACCACGCTGCCCCACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGC

*****
P_AAF44220      601
CCTCTCAGACCACGCTGCCCCACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGC

ss.DNA59820      661
TGGAGCGTGTGGTGTTCCTGACGGGCGCACGGGGCCGCCGGGCCCCACCTGGCATGGCAG

*****
P_AAF44220      661
TGGAGCGTGTGGTGTTCCTGACGGGCGCACGGGGCCGCCGGGCCCCACCTGGCATGGCAG

ss.DNA59820      721
TGGTGACGCTGGGCGAGGAGCGACCCATTGGACACCTGCACCTGGCGCTGCGCCACCTGC

*****
P_AAF44220      721
TGGTGACGCTGGGCGAGGAGCGACCCATTGGACACCTGCACCTGGCGCTGCGCCACCTGC

ss.DNA59820      781
TGGAGCAGCACGGCGACGACTTTGACTGGTTCTTCCTGGTGCCTGACACCACCTACACCG

*****
P_AAF44220      781
TGGAGCAGCACGGCGACGACTTTGACTGGTTCTTCCTGGTGCCTGACACCACCTACACCG

ss.DNA59820      841
AGGCGCACGGCCTGGCACGCCTAACTGGCCACCTCAGCCTGGCCTCCGCCGCCACCTGT

*****
P_AAF44220      841
AGGCGCACGGCCTGGCACGCCTAACTGGCCACCTCAGCCTGGCCTCCGCCGCCACCTGT

ss.DNA59820      901
ACCTGGGCGGGCCCCAGGACTTCATCGGCGGAGAGCCCCACCCCGGCCGCTACTGCCACG

*****
P_AAF44220      901
ACCTGGGCGGGCCCCAGGACTTCATCGGCGGAGAGCCCCACCCCGGCCGCTACTGCCACG

ss.DNA59820      961

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BLAST RESULTS A-0

GAGGCTTTGGGGTGCTGCTGTCGCGCATGCTGCTGCAACAACCTGCGCCCCACCTGGAAG

P_AAF44220 961

GAGGCTTTGGGGTGCTGCTGTCGCGCATGCTGCTGCAACAACCTGCGCCCCACCTGGAAG

ss.DNA59820 1021

GCTGCCGCAACGACATCGTCAGTGCGCGCCCTGACGAGTGGCTGGGTGCTGCATTCTCG

P_AAF44220 1021

GCTGCCGCAACGACATCGTCAGTGCGCGCCCTGACGAGTGGCTGGGTGCTGCATTCTCG

ss.DNA59820 1081

ATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGGGGGTGCACTATAGCCATCTGGAGC

P_AAF44220 1081

ATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGGGGGTGCACTATAGCCATCTGGAGC

ss.DNA59820 1141

TGAGCCCTGGGGAGCCAGTGCAGGAGGGGGACCCTCATTTCCGAAGTGCCCTGACAGCCC

P_AAF44220 1141

TGAGCCCTGGGGAGCCAGTGCAGGAGGGGGACCCTCATTTCCGAAGTGCCCTGACAGCCC

ss.DNA59820 1201

ACCCTGTGCGTGACCCTGTGCACATGTACCAGCTGCACAAAGCTTCGCCCCGAGCTGAAC

P_AAF44220 1201

ACCCTGTGCGTGACCCTGTGCACATGTACCAGCTGCACAAAGCTTCGCCCCGAGCTGAAC

ss.DNA59820 1261

TGGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGATCCAGAATACCAGCCATC

P_AAF44220 1261

TGGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGATCCAGAATACCAGCCATC

ss.DNA59820 1321

TGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATTCCAGCACCATCCCGCC

P_AAF44220 1321

TGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATTCCAGCACCATCCCGCC

ss.DNA59820 1381

CGGCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCAGCACGCTTTCTCCT

P_AAF44220 1381

CGGCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCAGCACGCTTTCTCCT

ss.DNA59820 1441

GCGCCGATGGCTCACCCCGCTGCCACTGCGTGGGGCTGACCGGGCTGATGTGGCCGATG

P_AAF44220 1441

GCGCCGATGGCTCACCCCGCTGCCACTGCGTGGGGCTGACCGGGCTGATGTGGCCGATG

Blast Results A-9

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ss.DNA59820 1501
TTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCCGGCCTTGCGGCTCCAGA
*****
P_AAF44220 1501
TTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCCGGCCTTGCGGCTCCAGA

ss.DNA59820 1561
AGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGAATACACGC
*****
P_AAF44220 1561
AGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGAATACACGC

ss.DNA59820 1621
TGGACTTGACAGCTGGAGGCACTGACCCCCAGGGAGGCCGCCGCCCTCACTCGCCGAG
*****
P_AAF44220 1621
TGGACTTGACAGCTGGAGGCACTGACCCCCAGGGAGGCCGCCGCCCTCACTCGCCGAG

ss.DNA59820 1681
TGCAGCTGCTCCGGCCGCTGAGCCGCTGGAGATCTTGCCTGTGCCCTATGTCACTGAGG
*****
P_AAF44220 1681
TGCAGCTGCTCCGGCCGCTGAGCCGCTGGAGATCTTGCCTGTGCCCTATGTCACTGAGG

ss.DNA59820 1741
CCTCACGTCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGGCT
*****
P_AAF44220 1741
CCTCACGTCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGGCT

ss.DNA59820 1801
TCTTGGAGGCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC
*****
P_AAF44220 1801
TCTTGGAGGCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC

ss.DNA59820 1861
TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATGCAGATGTCTTCGCAC
*****
P_AAF44220 1861
TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATGCAGATGTCTTCGCAC

ss.DNA59820 1921
CTGTCAAGGCCACAGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGTGCCATGGC
*****
P_AAF44220 1921
CTGTCAAGGCCACAGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGTGCCATGGC

ss.DNA59820 1981
TCAGTGTGCAGACAGCCGCACCCTCACCCTGCGCCTCATGGATCTACTCTCCAAGAAGC
*****

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BLAST RESULTS A-10

P_AAF44220 1981
T̄CAGTGTGCAGACAGCCGCACCCTCACCCTGCGCCTCATGGATCTACTCTCCAAGAAGC

ss.DNA59820 2041
ACCCGCTGGACACACTGTTCTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCC

P_AAF44220 2041
ĀCCCGCTGGACACACTGTTCTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCC

ss.DNA59820 2101
TGAACCGCTGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTCC

P_AAF44220 2101
T̄GAACCGCTGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTCC

ss.DNA59820 2161
AAGCCTTCCACCCAGGTGTGGCCCCACCACAAGGGCCTGGGCCCCCAGAGCTGGGCCGTG

P_AAF44220 2161
ĀAGCCTTCCACCCAGGTGTGGCCCCACCACAAGGGCCTGGGCCCCCAGAGCTGGGCCGTG

ss.DNA59820 2221
ACACTGGCCGCTTTGATCGCCAGGCAGCCAGCGAGGCCTGCTTCTACAACCTCCGACTACG

P_AAF44220 2221
ĀCACTGGCCGCTTTGATCGCCAGGCAGCCAGCGAGGCCTGCTTCTACAACCTCCGACTACG

ss.DNA59820 2281
TGGCAGCCCGTGGGCGCCTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCC

P_AAF44220 2281
T̄GGCAGCCCGTGGGCGCCTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCC

ss.DNA59820 2341
TGGATGTGTACGAGCTGTTCTCCTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGC

P_AAF44220 2341
T̄GGATGTGTACGAGCTGTTCTCCTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGC

ss.DNA59820 2401
CGGCGCTGCTGCAGCGCTACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGT

P_AAF44220 2401
C̄GGCGCTGCTGCAGCGCTACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGT

ss.DNA59820 2461
ACCACCGCTGCCTCCAGAGCGTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGC

P_AAF44220 2461
ĀCCACCGCTGCCTCCAGAGCGTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGC

ss.DNA59820 2521
TACTCTTTGAACAGGAGCAGGGCAACAGCACCTGACCCACCCCTGTCCCCGTGGGCCGTG

BLAST RESULTS A-II

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*****
P_AAF44220 2521
TACTCTTTGAACAGGAGCAGGGCAACAGCACCTGACCCACCCCTGTCCCCGTGGGCCGTG

ss.DNA59820 2581
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*****
P_AAF44220 2581
GCATGGCCACACCCACCCCACTTCTCCCCAAAACCAGAGCCACCTGCCAGCCTCGCTG

ss.DNA59820 2641
GGCAGGGCTGGCCGTAGCCAGACCCCAAGCTGGCCCACTGGTCCCCTCTCTGGCTCTGTG

*****
P_AAF44220 2641
GGCAGGGCTGGCCGTAGCCAGACCCCAAGCTGGCCCACTGGTCCCCTCTCTGGCTCTGTG

ss.DNA59820 2701
GGTCCCTGGGCTCTGGACAAGCACTGGGGGACGTGCCCCAGAGCCACCCACTTCTCATC

*****
P_AAF44220 2701
GGTCCCTGGGCTCTGGACAAGCACTGGGGGACGTGCCCCAGAGCCACCCACTTCTCATC

ss.DNA59820 2761
CCAAACCCAGTTTCCCTGCCCCCTGACGCTGCTGATTGCGGCTGTGGCCTCCACGTATTT

*****
P_AAF44220 2761
CCAAACCCAGTTTCCCTGCCCCCTGACGCTGCTGATTGCGGCTGTGGCCTCCACGTATTT

ss.DNA59820 2821
ATGCAGTACAGTCTGCCTGACGCCAGCCCTGCCTCTGGGCCCTGGGGGCTGGGCTGTAGA

*****
P_AAF44220 2821
ATGCAGTACAGTCTGCCTGACGCCAGCCCTGCCTCTGGGCCCTGGGGGCTGGGCTGTAGA

ss.DNA59820 2881
AGAGTTGTTGGGGAAGGAGGGAGCTGAGGAGGGGGCATCTCCCAACTTCTCCCTTTTGGA

*****
P_AAF44220 2881
AGAGTTGTTGGGGAAGGAGGGAGCTGAGGAGGGGGCATCTCCCAACTTCTCCCTTTTGGA

ss.DNA59820 2941 CCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCAAGTGTGGAAAAA
*****
P_AAF44220 2941 CCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCAAGTGTGGAAAAA

>3 P_AAC58388 Human PRO1281 nucleotide sequence SEQ ID NO:56. (2987 bp)
[1 seg]
Score = 2980 (5907 bits), Expect = 0.0
Identities = 2987/2988 (99%), Gaps = 1/2988 (0%), at 1,1-2988,2987,
Strand +/+

ss.DNA59820 1
GCCGAGCGCAAGAACCCTGCGCAGCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGC

*****

```

P_AAC58388 1
G_CCGAGCGCAAGAACCCTGCGCAGCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGC

ss.DNA59820 61
TCCGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCCGC

P_AAC58388 61
T_CCGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCCGC

ss.DNA59820 121
GGGGCCCGAGCCCTCCGGATCCGCCCCCTCCCGGTCCCGCCCCCTCGGAGACTCCTCTG

P_AAC58388 121
G_GGGCCCGAGCCCTCCGGATCCGCCCCCTCCCGGTCCCGCCCCCTCGGAGACTCCTCTG

ss.DNA59820 181
GCTGCTCTGGGGGTTCCGCCGGGGCCGGGGACCCGCGGTCCGGGCGCCATGCGGGCATCGC

P_AAC58388 181
G_CTGCTCTGGGGGTTCCGCCGGGGCCGGGGACCCGCGGTCCGGGCGCCATGCGGGCATCGC

ss.DNA59820 241
TGCTGCTGTCTGGTGTCTGCGGCCCCGAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTCA

P_AAC58388 241
T_GCTGCTGTCTGGTGTCTGCGGCCCCGAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTCA

ss.DNA59820 301
CCCTGAGCCTGCTCAGCGTCACCTGGGTGGAGGAGCCGTGCGGCCCAGGCCCCGCCCAAC

P_AAC58388 301
C_CCTGAGCCTGCTCAGCGTCACCTGGGTGGAGGAGCCGTGCGGCCCAGGCCCCGCCCAAC

ss.DNA59820 361
CTGGAGACTCTGAGCTGCCGCCGCGCGGCAACACCAACGCGGCGCGCCGGCCCAACTCGG

P_AAC58388 361
C_TGGAGACTCTGAGCTGCCGCCGCGCGGCAACACCAACGCGGCGCGCCGGCCCAACTCGG

ss.DNA59820 421
TGCAGCCCGGAGCGGAGCGCGAGAAGCCCGGGGCGGCGAAGGCGCCGGGGAGAATTGGG

P_AAC58388 421
T_GCAGCCCGGAGCGGAGCGCGAGAAGCCCGGGGCGGCGAAGGCGCCGGGGAGAATTGGG

ss.DNA59820 481
AGCCGCGCGTCTTGCCCTACCACCCTGCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTCA

P_AAC58388 481
A_GCCGCGCGTCTTGCCCTACCACCCTGCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTCA

ss.DNA59820 541
GGACCCGCTACATCAGCACGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGA

BLAST RESULTS A13

```

*****
P_AAC58388      541
GGACCCGCTACATCAGCACGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGA

ss.DNA59820      601
CCTCTCAGACCACGCTGCCCCACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGC

*****
P_AAC58388      601
CCTCTCAGACCACGCTGCCCCACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGC

ss.DNA59820      661
TGGAGCGTGTGGTGTTCCTGACGGGCGCACGGGGCCGCCGGGCCCCACCTGGCATGGCAG

*****
P_AAC58388      661
TGGAGCGTGTGGTGTTCCTGACGGGCGCACGGGGCCGCCGGGCCCCACCTGGCATGGCAG

ss.DNA59820      721
TGGTGACGCTGGGCGAGGAGCGACCCATTGGACACCTGCACCTGGCGCTGCGCCACCTGC

*****
P_AAC58388      721
TGGTGACGCTGGGCGAGGAGCGACCCATTGGACACCTGCACCTGGCGCTGCGCCACCTGC

ss.DNA59820      781
TGGAGCAGCACGGCGACGACTTTGACTGGTTCTTCCTGGTGCCTGACACCACCTACACCG

*****
P_AAC58388      781
TGGAGCAGCACGGCGACGACTTTGACTGGTTCTTCCTGGTGCCTGACACCACCTACACCG

ss.DNA59820      841
AGGCGCACGGCCTGGCACGCCTAACTGGCCACCTCAGCCTGGCCTCCGCCGCCACCTGT

*****
P_AAC58388      841
AGGCGCACGGCCTGGCACGCCTAACTGGCCACCTCAGCCTGGCCTCCGCCGCCACCTGT

ss.DNA59820      901
ACCTGGGCGCGCCCCAGGACTTCATCGGCGGAGAGCCACCCCCGGCCGCTACTGCCACG

*****
P_AAC58388      901
ACCTGGGCGCGCCCCAGGACTTCATCGGCGGAGAGCCACCCCCGGCCGCTACTGCCACG

ss.DNA59820      961
GAGGCTTTGGGGTGCTGCTGTCGCGCATGCTGCTGCAACAACTGCGCCCCACCTGGAAG

*****
P_AAC58388      961
GAGGCTTTGGGGTGCTGCTGTCGCGCATGCTGCTGCAACAACTGCGCCCCACCTGGAAG

ss.DNA59820     1021
GCTGCCGCAACGACATCGTCAGTGC GCGCCCTGACGAGTGGCTGGGTGCTGCATTCTCG

*****
P_AAC58388     1021
GCTGCCGCAACGACATCGTCAGTGC GCGCCCTGACGAGTGGCTGGGTGCTGCATTCTCG

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BLAST RESULTS A-1A

```

ss.DNA59820 1081
ATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGGGGGTGCCTATAGCCATCTGGAGC
*****
P_AAC58388 1081
ATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGGGGGTGCCTATAGCCATCTGGAGC

ss.DNA59820 1141
TGAGCCCTGGGGAGCCAGTGCAGGAGGGGGACCCTCATTTCCGAAGTGCCCTGACAGCCC
*****
P_AAC58388 1141
TGAGCCCTGGGGAGCCAGTGCAGGAGGGGGACCCTCATTTCCGAAGTGCCCTGACAGCCC

ss.DNA59820 1201
ACCCTGTGCGTGACCCTGTGCACATGTACCAGCTGCACAAAGCTTTGCCCCGAGCTGAAC
*****
P_AAC58388 1201
ACCCTGTGCGTGACCCTGTGCACATGTACCAGCTGCACAAAGCTTTGCCCCGAGCTGAAC

ss.DNA59820 1261
TGGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGATCCAGAATACCAGCCATC
*****
P_AAC58388 1261
TGGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGATCCAGAATACCAGCCATC

ss.DNA59820 1321
TGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATTCCAGCACCATCCCGCC
*****
P_AAC58388 1321
TGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATTCCAGCACCATCCCGCC

ss.DNA59820 1381
CGGCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCAGCACGCTTTCTCCT
*****
P_AAC58388 1381
CGGCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCAGCACGCTTTCTCCT

ss.DNA59820 1441
GCGCCGATGGCTCACCCCGCTGCCCACTGCGTGGGGCTGACCGGGCTGATGTGGCCGATG
*****
P_AAC58388 1441
GCGCCGATGGCTCACCCCGCTGCCCACTGCGTGGGGCTGACCGGGCTGATGTGGCCGATG

ss.DNA59820 1501
TTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCCGGCCTTGCGGCTCCAGA
*****
P_AAC58388 1501
TTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCCGGCCTTGCGGCTCCAGA

ss.DNA59820 1561
AGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGAATACACGC
*****
P_AAC58388 1561

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BLAST RESULTS A-15

AGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCCGGGGTATGGAATACACGC

ss.DNA59820 1621
TGGACTTGACAGCTGGAGGCACTGACCCCCCAGGGAGGCCGCCGGCCCCCTCACTCGCCGAG

P_AAC58388 1621
TGGACTTGACAGCTGGAGGCACTGACCCCCCAGGGAGGCCGCCGGCCCCCTCACTCGCCGAG

ss.DNA59820 1681
TGCAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCCTGTGCCCTATGTCACTGAGG

P_AAC58388 1681
TGCAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCCTGTGCCCTATGTCACTGAGG

ss.DNA59820 1741
CCTCACGTCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGGCT

P_AAC58388 1741
CCTCACGTCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGGCT

ss.DNA59820 1801
TCTTGGAGGCCCTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC

P_AAC58388 1801
TCTTGGAGGCCCTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC

ss.DNA59820 1861
TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGGCCCATGCAGATGTCTTCGCAC

P_AAC58388 1861
TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGGCCCATGCAGATGTCTTCGCAC

ss.DNA59820 1921
CTGTCAAGGCCCACGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGGTGCCATGGC

P_AAC58388 1921
CTGTCAAGGCCCACGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGGTGCCATGGC

ss.DNA59820 1981
TCAGTGTGCAGACAGCCGCACCCTCACCCTGCGCCTCATGGATCTACTCTCCAAGAAGC

P_AAC58388 1981
TCAGTGTGCAGACAGCCGCACCCTCACCCTGCGCCTCATGGATCTACTCTCCAAGAAGC

ss.DNA59820 2041
ACCCGCTGGACACACTGTTCCCTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCC

P_AAC58388 2041
ACCCGCTGGACACACTGTTCCCTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCC

ss.DNA59820 2101
TGAACCGCTGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTC

BLAST RESULTS A-W


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*****
P_AAC58388 2101
TGAACCGCTGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTCC

ss.DNA59820 2161
AAGCCTTCCACCCAGGTGTGGCCCCACCACAAGGGCCTGGGCCCCCAGAGCTGGGCCGTG

*****
P_AAC58388 2161
AAGCCTTCCACCCAGGTGTGGCCCCACCACAAGGGCCTGGGCCCCCAGAGCTGGGCCGTG

ss.DNA59820 2221
ACACTGGCCGCTTTGATCGCCAGGCAGCCAGCGAGGCCTGCTTCTACAACCTCCGACTACG

*****
P_AAC58388 2221
ACACTGGCCGCTTTGATCGCCAGGCAGCCAGCGAGGCCTGCTTCTACAACCTCCGACTACG

ss.DNA59820 2281
TGGCAGCCCGTGGGCGCCTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCC

*****
P_AAC58388 2281
TGGCAGCCCGTGGGCGCCTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCC

ss.DNA59820 2341
TGGATGTGTACGAGCTGTTCCCTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGC

*****
P_AAC58388 2341
TGGATGTGTACGAGCTGTTCCCTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGC

ss.DNA59820 2401
CGGCGCTGCTGCAGCGCTACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGT

*****
P_AAC58388 2401
CGGCGCTGCTGCAGCGCTACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGT

ss.DNA59820 2461
ACCACCGCTGCCTCCAGAGCGTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGC

*****
P_AAC58388 2461
ACCACCGCTGCCTCCAGAGCGTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGC

ss.DNA59820 2521
TACTCTTTGAACAGGAGCAGGGCAACAGCACCTGACCCACCCCTGTCCCCGTGGGCCGTG
*****
*****
P_AAC58388 2521 TACTCTTTGAACAGGAGCA-
GGCAACAGCACCTGACCCACCCCTGTCCCCGTGGGCCGTG

ss.DNA59820 2581
GCATGGCCACACCCACCCCACTTCTCCCCAAAACCAGAGCCACCTGCCAGCCTCGCTG

*****
P_AAC58388 2580
GCATGGCCACACCCACCCCACTTCTCCCCAAAACCAGAGCCACCTGCCAGCCTCGCTG

ss.DNA59820 2641

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BLAST RESULTS A-17

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GGCAGGGCTGGCCGTAGCCAGACCCCAAGCTGGCCCACTGGTCCCCTCTCTGGCTCTGTG
*****
P_AAC58388 2640
GGCAGGGCTGGCCGTAGCCAGACCCCAAGCTGGCCCACTGGTCCCCTCTCTGGCTCTGTG

ss.DNA59820 2701
GGTCCCCTGGGCTCTGGACAAGCACTGGGGGACGTGCCCCCAGAGCCACCCACTTCTCATC
*****
P_AAC58388 2700
GGTCCCCTGGGCTCTGGACAAGCACTGGGGGACGTGCCCCCAGAGCCACCCACTTCTCATC

ss.DNA59820 2761
CCAAACCCAGTTTCCCTGCCCCCTGACGCTGCTGATTCTGGGCTGTGGCCTCCACGTATTT
*****
P_AAC58388 2760
CCAAACCCAGTTTCCCTGCCCCCTGACGCTGCTGATTCTGGGCTGTGGCCTCCACGTATTT

ss.DNA59820 2821
ATGCAGTACAGTCTGCCTGACGCCAGCCCTGCCTCTGGGCCCTGGGGGCTGGGCTGTAGA
*****
P_AAC58388 2820
ATGCAGTACAGTCTGCCTGACGCCAGCCCTGCCTCTGGGCCCTGGGGGCTGGGCTGTAGA

ss.DNA59820 2881
AGAGTTGTTGGGGAAGGAGGGAGCTGAGGAGGGGGCATCTCCCAACTTCTCCCTTTTGGGA
*****
P_AAC58388 2880
AGAGTTGTTGGGGAAGGAGGGAGCTGAGGAGGGGGCATCTCCCAACTTCTCCCTTTTGGGA

ss.DNA59820 2941 CCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCAAGTGTGGAAAAA
*****
P_AAC58388 2940 CCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCAAGTGTGGAAAAA

>4 P_AAC69800 Human breast tumour antigen coding sequence #2. (2514 bp)
[2 segs]
Score = 2487 (4930 bits), Expect = 0.0 [P_AAC69800, seg 1/2]
Identities = 2502/2507 (99%), at 482,1-2988,2507, Strand +/-

ss.DNA59820 482
GCCGCGCGTCTTGCCCTACCACCCTGCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTCAG
*****
P_AAC69800 1
GCCGCGCGTCTTGCCCTACCACCCTGCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTCAG

ss.DNA59820 542
GACCCGCTACATCAGCACGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGAC
*****
P_AAC69800 61
GACCCGCTACATCAGCACGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGAC

ss.DNA59820 602
CTCTCAGACCACGCTGCCCACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCT
*****

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BLAST RESULTS A-18

P_AAC69800 121
 CTCTCAGACCACGCTGCCACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACC GGCT

 ss.DNA59820 662
 GGAGCGTGTGGTGTTCCTGACGGGCGCACGGGGCCGCCGGGCCCCACCTGGCATGGCAGT

 P_AAC69800 181
 GGAGCGTGTGGTGTTCCTGACGGGCGCACGGGGCCGCCGGGCCCCACCTGGCATGGCAGT

 ss.DNA59820 722
 GGTGACGCTGGGCGAGGAGCGACCCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCT

 P_AAC69800 241
 GGTGACGCTGGGCGAGGAGCGACCCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCT

 ss.DNA59820 782
 GGAGCAGCACGGCGACGACTTTGACTGGTTCTTCCTGGTGCCTGACACCACCTACACCGA

 P_AAC69800 301
 GGAGCAGCACGGCGACGACTTTGACTGGTTCTTCCTGGTGCCTGACACCACCTACACCGA

 ss.DNA59820 842
 GGCGCACGGCCTGGCAGGCCTAACTGGCCACCTCAGCCTGGCCTCCGCCGCCACCTGTA

 P_AAC69800 361
 GGCGCACGGCCTGGCAGGCCTAACTGGCCACCTCAGCCTGGCCTCCGCCGCCACCTGTA

 ss.DNA59820 902
 CCTGGGCCGGCCCCAGGACTTCATCGGCGGAGAGCCCACCCCGGCCGCTACTGCCACGG

 P_AAC69800 421
 CCTGGGCCGGCCCCAGGACTTCATCGGCGGAGAGCCCACCCCGGCCGCTACTGCCACGG

 ss.DNA59820 962
 AGGCTTTGGGGTGCTGCTGTGCGCGCATGCTGCTGCAACAACCTGCGCCCCACCTGGAAGG

 P_AAC69800 481
 AGGCTTTGGGGTGCTGCTGTGCGCGCATGCTGCTGCAACAACCTGCGCCCCACCTGGAAGG

 ss.DNA59820 1022
 CTGCCGCAACGACATCGTCAGTGC GCGCCCTGACGAGTGGCTGGGTCGCTGCATTCTCGA

 P_AAC69800 541
 CTGCCGCAACGACATCGTCAGTGC GCGCCCTGACGAGTGGCTGGGTCGCTGCATTCTCGA

 ss.DNA59820 1082
 TGCCACCGGGGTGGGCTGCACTGGTGACCACGAGGGGGTGCACTATAGCCATCTGGAGCT

 P_AAC69800 601
 TGCCACCGGGGTGGGCTGCACTGGTGACCACGAGGGGGTGCACTATAGCCATCTGGAGCT

 ss.DNA59820 1142
 GAGCCCTGGGGAGCCAGTGCAGGAGGGGGACCCTCATTTCCGAAGTGCCCTGACAGCCCA

BLAST RESULTS A-19

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*****
P_AAC69800    661
GAGCCCTGGGGAGCCAGTGCAGGAGGGGGACCCTCATTTCCGAAGTGCCTGACAGCCCA

ss.DNA59820   1202
CCCTGTGCGTGACCCTGTGCACATGTACCAGCTGCACAAAGCTTTCGCCCCGAGCTGAACT

*****
P_AAC69800    721
CCCTGTGCGTGACCCTGTGCACATGTACCAGCTGCACAAAGCTTTCGCCCCGAGCTGAACT

ss.DNA59820   1262
GGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGATCCAGAATACCAGCCATCT

*****
P_AAC69800    781
GGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGATCCAGAATACCAGCCATCT

ss.DNA59820   1322
GGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATTCCAGCACCATCCCGCCC

*****
P_AAC69800    841
GGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATTCCAGCACCATCCCGCCC

ss.DNA59820   1382
GGCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCAGCAGCTTTCTCCTG
*****
*****
P_AAC69800    901
GGCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCAGCATGCTTTCTCCTG

ss.DNA59820   1442
CGCCGATGGCTCACCCCGCTGCCCCTGCGTGGGGCTGACCGGGCTGATGTGGCCGATGT

*****
P_AAC69800    961
CGCCGATGGCTCACCCCGCTGCCCCTGCGTGGGGCTGACCGGGCTGATGTGGCCGATGT

ss.DNA59820   1502
TCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCCGGCCTTGCGGCTCCAGAA

*****
P_AAC69800    1021
TCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCCGGCCTTGCGGCTCCAGAA

ss.DNA59820   1562
GCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGTATGGAATACACGCT

*****
P_AAC69800    1081
GCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGTATGGAATACACGCT

ss.DNA59820   1622
GGACTTGACGCTGGAGGCACTGACCCCCCAGGGAGGCCGCCGGCCCTCACTCGCCGAGT

*****
P_AAC69800    1141
GGACTTGACGCTGGAGGCACTGACCCCCCAGGGAGGCCGCCGGCCCTCACTCGCCGAGT

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BLAST RESULTS A-20

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ss.DNA59820 1682
GCAGCTGCTCCGGCCGCTGAGCCGCTGGAGATCTTGCTGTGCCCTATGTCACTGAGGC
*****
P_AAC69800 1201
GCAGCTGCTCCGGCCGCTGAGCCGCTGGAGATCTTGCTGTGCCCTATGTCACTGAGGC

ss.DNA59820 1742
CTCACGTCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGGCTT
*****
P_AAC69800 1261
CTCACGTCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGGCTT

ss.DNA59820 1802
CTTGAGGCGCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCCT
*****
P_AAC69800 1321
CTTGAGGCGCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCCT

ss.DNA59820 1862
GCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGCGCCATGCAGATGTCTTCGCACC
*****
P_AAC69800 1381
GCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGCGCCATGCAGATGTCTTCGCACC

ss.DNA59820 1922
TGTCAAGGCCACAGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGGTGCCATGGCT
*****
P_AAC69800 1441
TGTCAAGGCCACAGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGGTGCCATGGCT

ss.DNA59820 1982
CAGTGTGCAGACAGCCGACCCCTCACCCTGCGCCTCATGGATCTACTCTCCAAGAAGCA
*****
P_AAC69800 1501
CAGTGTGCAGACAGCCGACCCCTCACCCTACGCCTCATGGATCTACTCTCCAAGAAGCA

ss.DNA59820 2042
CCCCTGGACACACTGTTTCCTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCCT
*****
P_AAC69800 1561
CCCCTGGACACACTGTTTCCTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCCT

ss.DNA59820 2102
GAACCGCTGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTCCA
*****
P_AAC69800 1621
GAACCGCTGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTCCA

ss.DNA59820 2162
AGCCTTCCACCCAGGTGTGGCCCCACCACAAGGGCCTGGGCCCCCAGAGCTGGGCCGTGA
*****
P_AAC69800 1681

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BLAST RESULTS A-71

AGCCTTCCACCCAGCTGTGGCCCCACCACAAGGGCCTGGGCCCCCAGAGCTGGGCCGTGA

ss.DNA59820 2222
 CACTGGCCGCTTTGATCGCCAGGCAGCCAGCGAGGCCTGCTTCTACAACCTCCGACTACGT

 P_AAC69800 1741
 CACTGGCCGCTTTGATCGCCAGGCAGCCAGCGAGGCCTGCTTCTACAACCTCCGACTACGT

ss.DNA59820 2282
 GGCAGCCCGTGGGCGCCTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCCT

 P_AAC69800 1801
 GGCAGCCCGTGGGCGCCTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCCT

ss.DNA59820 2342
 GGATGTGTACGAGCTGTTCCCTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCC

 P_AAC69800 1861
 GGATGTGTACGAGCTGTTCCCTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCC

ss.DNA59820 2402
 GCGCTGCTGCAGCGCTACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGTA

 P_AAC69800 1921
 GCGCTGCTGCAGCGCTACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGTA

ss.DNA59820 2462
 CCACCGCTGCCTCCAGAGCGTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGCT

 P_AAC69800 1981
 CCACCGCTGCCTCCAGAGCGTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGCT

ss.DNA59820 2522
 ACTCTTTGAACAGGAGCAGGGCAACAGCACCTGACCCACCCCTGTCCCCGTGGGCCGTGG

 P_AAC69800 2041
 ACTCTTTGAACAGGAGCAGGGCAACAGCACCTGACCCACCCCTGTCCCCGTGGGCCGTGG

ss.DNA59820 2582
 CATGGCCACACCCACCCCACTTCTCCCCAAAACCAGAGCCACCTGCCAGCCTCGCTGG

 P_AAC69800 2101
 CATGGCCACACCCACCCCACTTCTCCCCAAAACCAGAGCCACCTGCCAGCCTCGCTGG

ss.DNA59820 2642
 GCAGGGCTGGCCGTAGCCAGACCCCAAGCTGGCCCACTGGTCCCCTCTCTGGCTCTGTGG

 P_AAC69800 2161
 GCAGGGCTGGCCGTAGCCAGACCCCAAGCTGGCCCACTGGTCCCCTCTCTGGCTCTGTGG

ss.DNA59820 2702
 GTCCCTGGGCTCTGGACAAGCACTGGGGGACGTGCCCCAGAGCCACCCACTTCTCATCC

BLAST RESULTS A-22

```

*****
P_AAC69800 2221
GTCCCTGGGCTCTGGACAAGCACTGGGGGACGTGCCCCAGAGCCACCCACTTCTCATCC

ss.DNA59820 2762
CAAACCCAGTTTCCCTGCCCCCTGACGCTGCTGATTCTGGGCTGTGGCCTCCACGTATTTA

*****
P_AAC69800 2281
CAAACCCAGTTTCCCTGCCCCCTGACGCTGCTGATTCTGGGCTGTGGCCTCCACGTATTTA

ss.DNA59820 2822
TGCAGTACAGTCTGCCTGACGCCAGCCCTGCCTCTGGGCCCTGGGGGCTGGGCTGTAGAA

*****
P_AAC69800 2341
TGCAGTACAGTCTGCCTGACGCCAGCCCTGCCTCTGGGCCCTGGGGGCTGGGCTGTAGAA

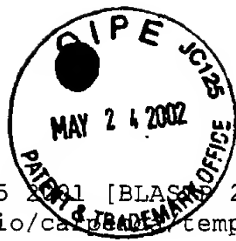
ss.DNA59820 2882
GAGTTGTTGGGGAAGGAGGGAGCTGAGGAGGGGGCATCTCCCAACTTCTCCCTTTTGGAC

*****
P_AAC69800 2401
GAGTTGTTGGGGAAGGAGGGAGCTGAGGAGGGGGCATCTCCCAACTTCTCCCTTTTGGAC

ss.DNA59820 2942 CCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCAAGTGTGGAAAAA
*****
P_AAC69800 2461 CCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCAAGTGTGAAAAAA

```

BLAST RES VUTS A-23



(P)

Wed Nov 21 09:32:25 2001 [BLAST 2.2.1 [Jul-12-2001], NCBI]
/home/ruby/va/Molbio/cap/blast/tempblast/pl.DNA59820.nc (775 aa)

Sequences producing High-scoring Segment Pairs:	Score	Match	Pct	E-val
1 P_AAB65252 Human PRO1281 (UNQ651) protein sequence S	4074	775	100	0.0
2 P_AAY66729 Membrane-bound protein PRO1281 - Homo sap	4074	775	100	0.0
3 P_AAB24078 Human PRO1281 protein sequence SEQ ID NO:	4074	775	100	0.0

>1 P_AAB65252 Human PRO1281 (UNQ651) protein sequence SEQ ID NO:326 - Homo (775 aa) [1 seg]

Score = 4074 (1573 bits), Expect = 0.0

Identities = 775/775 (100%), Positives = 775/775 (100%), at 1,1-775,775

DNA59820.nc	1	MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAAR
P_AAB65252	1	MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAAR
DNA59820.nc	61	RPNSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRL
P_AAB65252	61	RPNSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRL
DNA59820.nc	121	VAVLTSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLA
P_AAB65252	121	VAVLTSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLA
DNA59820.nc	181	LRHLLEQHGDDFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPG
P_AAB65252	181	LRHLLEQHGDDFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPG
DNA59820.nc	241	RYCHGGFGVLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHY
P_AAB65252	241	RYCHGGFGVLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHY
DNA59820.nc	301	SHLELSPGEPVQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAELERTYQEIQELQWEIQ
P_AAB65252	301	SHLELSPGEPVQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAELERTYQEIQELQWEIQ
DNA59820.nc	361	NTSHLAVDGDRAAAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRA
P_AAB65252	361	NTSHLAVDGDRAAAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRA
DNA59820.nc	421	DVADVLGTALEELNRRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPOGGRRP
P_AAB65252	421	DVADVLGTALEELNRRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPOGGRRP
DNA59820.nc	481	LTRRVQLLRPLSRVEILVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAA
P_AAB65252	481	LTRRVQLLRPLSRVEILVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAA
P_AAB65252	541	AALTLLLLYEPRQAQRVAHADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDL
DNA59820.nc	601	LSKKHPLDTLFLLAGPDTVLTDPDFLNRCRMHAISGWQAFFPMHFQAFHGPVAPPQGGPPP
P_AAB65252	601	LSKKHPLDTLFLLAGPDTVLTDPDFLNRCRMHAISGWQAFFPMHFQAFHGPVAPPQGGPPP

BLAST RESULTS B-1

DNA59820.nc 661 ELGRDTGRFDRQAASEACFYNSDYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVL

 P_AAB65252 661 ELGRDTGRFDRQAASEACFYNSDYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVL

DNA59820.nc 721 RAVEPALLQRYRAQTCSARLSEDLYHRCLQSVLEGLGSRQTQLAMLLFEQEQGNST

 P_AAB65252 721 RAVEPALLQRYRAQTCSARLSEDLYHRCLQSVLEGLGSRQTQLAMLLFEQEQGNST

>2 P_AAY66729 Membrane-bound protein PRO1281 - Homo sapiens. (775 aa) [1 seg]
 Score = 4074 (1573 bits), Expect = 0.0
 Identities = 775/775 (100%), Positives = 775/775 (100%), at 1,1-775,775

DNA59820.nc 1 MRASLLLSVLRPAGPVAVGISLGF TLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAAR

 P_AAY66729 1 MRASLLLSVLRPAGPVAVGISLGF TLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAAR

DNA59820.nc 61 RPNSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRL

 P_AAY66729 61 RPNSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRL

DNA59820.nc 121 VAVLTSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLA

 P_AAY66729 121 VAVLTSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLA

DNA59820.nc 181 LRHLLEQHGD DFWFLVPD TTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPG

 P_AAY66729 181 LRHLLEQHGD DFWFLVPD TTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPG

DNA59820.nc 241 RYCHGGFGVLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGR CILDATGVGCTGDHEGVHY

 P_AAY66729 241 RYCHGGFGVLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGR CILDATGVGCTGDHEGVHY

DNA59820.nc 301 SHLELSPGEPVQEGDPHFRSALT AHPVRDPVHMYQLHKAFARAE LERTYQEIQELQWEIQ

 P_AAY66729 301 SHLELSPGEPVQEGDPHFRSALT AHPVRDPVHMYQLHKAFARAE LERTYQEIQELQWEIQ

DNA59820.nc 361 NTSHLAVDGDRAAAWPGV I PAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRA

 P_AAY66729 361 NTSHLAVDGDRAAAWPGV I PAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRA

DNA59820.nc 421 DVADVLTAL EELNRRYHPALRLQKQQLVNGYRRFDPARGMEY TLDLQLEALTPQGGRRP

 P_AAY66729 421 DVADVLTAL EELNRRYHPALRLQKQQLVNGYRRFDPARGMEY TLDLQLEALTPQGGRRP

DNA59820.nc 481 LTRRVQLLRPLSRVEILPV PYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAA

 P_AAY66729 481 LTRRVQLLRPLSRVEILPV PYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAA

DNA59820.nc 541 AALTLLLLYEPRQAQRVAHADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDL

 P_AAY66729 541 AALTLLLLYEPRQAQRVAHADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDL

DNA59820.nc 601 LSKKHPLD TLFLLAGPD T VLT P DFLNRCRMHAISGWQAFFPMHFQAFH PGVAPPQGP GPP

 P_AAY66729 601 LSKKHPLD TLFLLAGPD T VLT P DFLNRCRMHAISGWQAFFPMHFQAFH PGVAPPQGP GPP

BLAST RESULTS B-2

DNA59820.nc 661 ELGRDTGRFDRQAASEACFYNSDYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVL

P_AAY66729 661 ELGRDTGRFDRQAASEACFYNSDYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVL

DNA59820.nc 721 RAVEPALLQRYRAQTCSARLSEDLYHRCLQSVLEGLGSRTQLAMLLFEQEQGNST

P_AAY66729 721 RAVEPALLQRYRAQTCSARLSEDLYHRCLQSVLEGLGSRTQLAMLLFEQEQGNST

>3 P_AAB24078 Human PRO1281 protein sequence SEQ ID NO:57 - Homo sapiens. (775
aa) [1 seg]
Score = 4074 (1573 bits), Expect = 0.0
Identities = 775/775 (100%), Positives = 775/775 (100%), at 1,1-775,775

DNA59820.nc 1 MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAAR

P_AAB24078 1 MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAAR

DNA59820.nc 61 RPNSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRL

P_AAB24078 61 RPNSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRL

DNA59820.nc 121 VAVLTSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLA

P_AAB24078 121 VAVLTSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLA

DNA59820.nc 181 LRHLLEQHGDDFDWFFLVPDITYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPG

P_AAB24078 181 LRHLLEQHGDDFDWFFLVPDITYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPG

DNA59820.nc 241 RYCHGGFGVLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHY

P_AAB24078 241 RYCHGGFGVLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHY

DNA59820.nc 301 SHLELSPGEPVQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAEELERTYQEIQELQWEIQ

P_AAB24078 301 SHLELSPGEPVQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAEELERTYQEIQELQWEIQ

DNA59820.nc 361 NTSHLAVDGDRAAAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRA

P_AAB24078 361 NTSHLAVDGDRAAAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRA

DNA59820.nc 421 DVADVLGTALEELNRRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRP

P_AAB24078 421 DVADVLGTALEELNRRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRP

DNA59820.nc 481 LTRRVQLLRPLSRVEILVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAA

P_AAB24078 481 LTRRVQLLRPLSRVEILVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAA

DNA59820.nc 541 AALTLLLLYEPRQAQRVAHADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDL

P_AAB24078 541 AALTLLLLYEPRQAQRVAHADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDL

DNA59820.nc 601 LSKKHPLDTLFLLAGPDTVLTDPFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPGPP

P_AAB24078 601 LSKKHPLDTLFLLAGPDTVLTDPFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPGPP

BLAST RESULTS B-3

DNA59820.nc 661 ELGRDTGRFDRQAASEACFYNSDYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVL

P_AAB24078 661 ELGRDTGRFDRQAASEACFYNSDYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVL

DNA59820.nc 721 RAVEPALLQRYRAQTCSARLSEDLYHRCLQSVLEGLGSRTQLAMLLFEQEQGNST

P_AAB24078 721 RAVEPALLQRYRAQTCSARLSEDLYHRCLQSVLEGLGSRTQLAMLLFEQEQGNST

BLAST RESULTS B-A